

## SEQUENCE LISTING

<110> MASURE, STEFAN  
RICHARDSON, ALAN

<120> HUMAN AKT-3

<130> JAB-1458

<140> 09/869,079

<141> 1999-12-17

<150> PCT/GB99/04311

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<160> 16

<170> PatentIn Ver. 3.2

<210> 1

<211> 1547

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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&lt;210&gt; 3

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
      35              40              45

Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
      50              55              60

Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
      65              70              75              80

Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
      85              90              95

Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
      100              105              110

Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
      115              120              125

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Gly	Glu	Glu	Glu	Met	Asp	Ala	Ser	Thr	Thr	His	His	Lys	Arg	Lys	Thr	130	135	140
Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	145	150	155
Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Tyr	Ala	Met	165	170	175
Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	Glu	Val	Ala	His	180	185	190
Thr	Leu	Thr	Glu	Ser	Arg	Val	Leu	Lys	Asn	Thr	Arg	His	Pro	Phe	Leu	195	200	205
Thr	Ser	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	Lys	Asp	Arg	Leu	Cys	Phe	Val	210	215	220
Met	Glu	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	225	230	235
Arg	Val	Phe	Ser	Glu	Asp	Arg	Thr	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	245	250	255
Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Gly	Lys	Ile	Val	Tyr	Arg	Asp	Leu	260	265	270
Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	275	280	285
Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Thr	Asp	Ala	Ala	Thr	Met	Lys	290	295	300
Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	305	310	315
Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	325	330	335
Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	340	345	350
Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Asp	Ile	Lys	Phe	Pro	Arg	Thr	355	360	365
Leu	Ser	Ser	Asp	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Ile	Lys	Asp	370	375	380
Pro	Asn	Lys	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	Glu	Ile	Met	385	390	395
Arg	His	Ser	Phe	Phe	Ser	Gly	Val	Asn	Trp	Gln	Asp	Val	Tyr	Asp	Lys	405	410	415
Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	420	425	430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro  
 435 440 445

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Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
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<210> 4

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<210> 5

<211> 25

<212> DNA

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<210> 6

<211> 26

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<210> 7

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<210> 10  
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<223> Description of Artificial Sequence: Synthetic  
primer

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<210> 12  
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 <213> Homo sapiens

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<210> 14  
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24

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 <213> Homo sapiens

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                     20                    25                    30  
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg  
                     35                    40                    45  
 Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys  
     50                    55                    60

Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	Ile	Ile	Arg	Cys	Leu	Gln	Trp	65	70	75	80
Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Glu	Thr	Pro	Glu	Glu	Arg	85	90	95	
Glu	Glu	Trp	Thr	Thr	Ala	Ile	Gln	Thr	Val	Ala	Asp	Gly	Leu	Lys	Lys	100	105	110	
Gln	Glu	Glu	Glu	Glu	Met	Asp	Phe	Arg	Ser	Gly	Ser	Pro	Ser	Asp	Asn	115	120	125	
Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser	Leu	Ala	Lys	Pro	Lys	His	Arg	130	135	140	
Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	145	150	155	160
Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	165	170	175	
Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Val	Ala	Lys	Asp	Glu	Val	180	185	190	
Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	Leu	Gln	Asn	Ser	Arg	His	Pro	195	200	205	
Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	His	Asp	Arg	Leu	Cys	210	215	220	
Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	225	230	235	240
Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	245	250	255	
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Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	275	280	285	
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Lys	Asp	Gly	Ala	290	295	300	
Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	305	310	315	320
Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	325	330	335	
Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	340	345	350	
Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe	355	360	365	

Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu  
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 Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys  
 385 390 395 400  
 Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val  
 405 410 415  
 Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu  
 420 425 430  
 Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr  
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 Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala  
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<210> 16  
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 Gly Ser Phe Ile Gly Tyr Lys Glu Arg Pro Glu Ala Pro Asp Gln Thr  
 35 40 45  
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 50 55 60  
 Thr Glu Arg Pro Arg Pro Asn Thr Phe Val Ile Arg Cys Leu Gln Trp  
 65 70 75 80  
 Thr Thr Val Ile Glu Arg Thr Phe His Val Asp Ser Pro Asp Glu Arg  
 85 90 95  
 Glu Glu Trp Met Arg Ala Ile Gln Met Val Ala Asn Ser Leu Lys Gln  
 100 105 110  
 Arg Ala Pro Gly Glu Asp Pro Met Asp Tyr Lys Cys Gly Ser Pro Ser  
 115 120 125  
 Asp Ser Ser Thr Thr Glu Glu Met Glu Val Ala Val Ser Lys Ala Arg  
 130 135 140



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				165					170					175		
Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	
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Tyr	Arg	Asp	Ile	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	
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Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Ser	Asp	Gly	
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Lys	Glu	Val	Met	Glu	His	Arg	Phe	Phe	Leu	Ser	Ile	Asn	Trp	Gln	Asp	
				405					410					415		
Val	Val	Gln	Lys	Lys	Leu	Leu	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	
				420				425					430			
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		435					440					445				

Thr Ile Thr Pro Pro Asp Arg Tyr Asp Ser Leu Gly Leu Leu Glu Leu  
450 455 460

Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg  
465 470 475 480

Glu